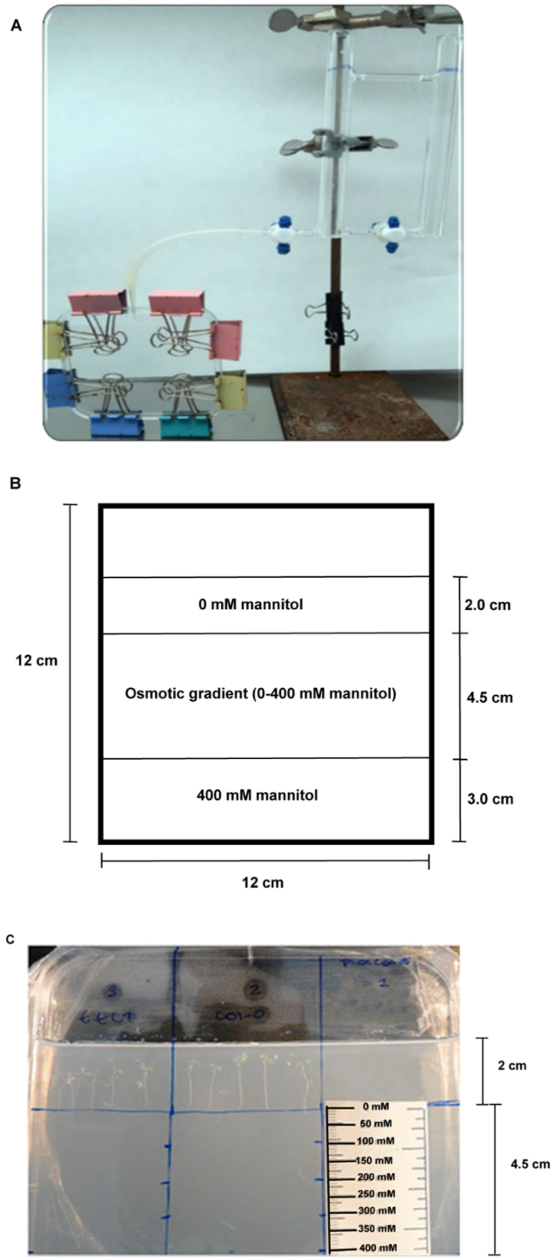
Supplementary Material

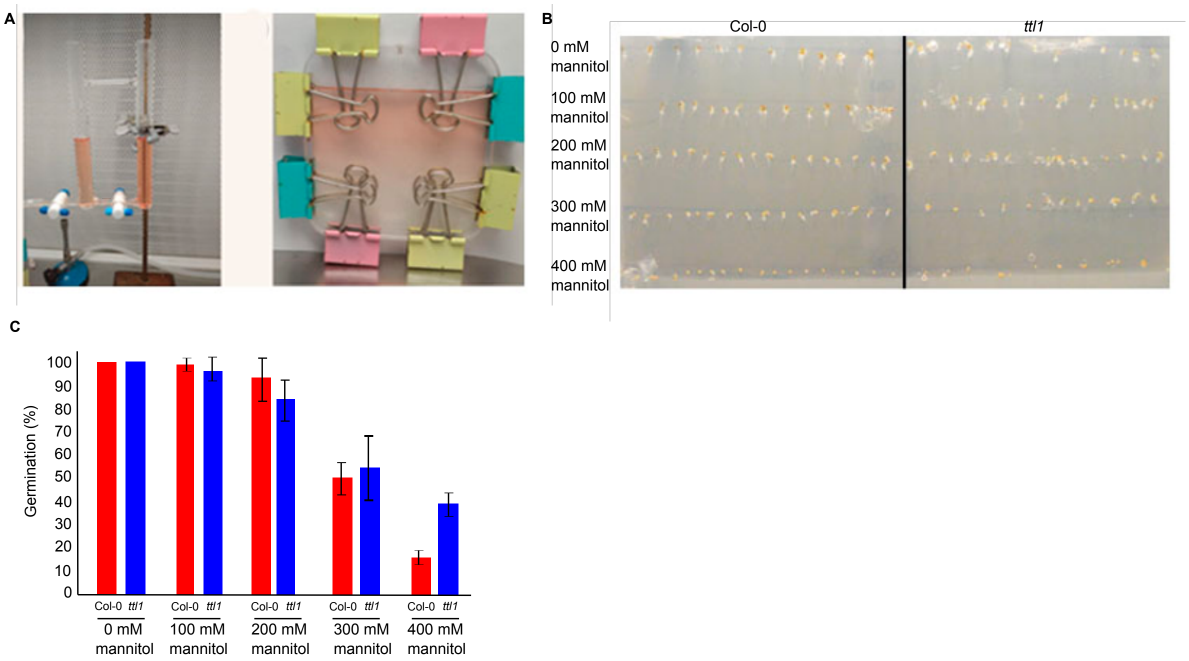
1 Supplementary Figures and Tables

1.1 Supplementary Figures

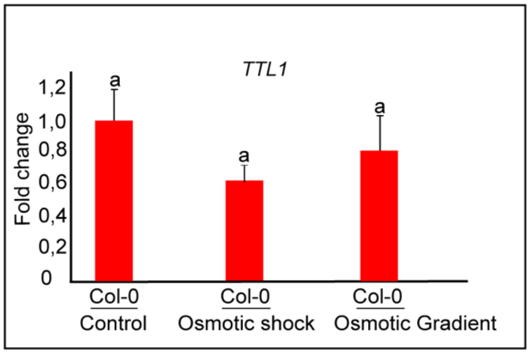


Supplemental Figure 1. System used to establish the osmotic gradient. **A.** Gradient maker. **B.** Vertical acrylic plate. **C.** Representative schematic of a Petri dish containing the osmotic gradient.

Sequentially, 1 block of medium with 400 mM mannitol (3.0 cm), 1 block of medium with osmotic gradient (4.5 cm), and 1 block of medium without mannitol (2.0 cm) were placed.



Supplemental Figure 2. Image depicting how seedlings were planted in the osmotic gradient system. Seedlings are placed in 0 mM mannitol, and the root tips are positioned at the entry to the gradient. The ruler is shown, correlating mannitol concentrations with osmotic potentials measured using the OSMOMAT 030 osmometer model (Gonotech, Berlin, Germany).



Supplemental Figure 3. *TTL1* expression levels in roots of Col-0 grown in control, osmotic shock and osmotic gradient conditions. Data are presented as means ± standard deviation (SD). Three biological replicates and two technical replicates were considered, and gene expression is relative to *CYTOCHROME C OXIDASE RELATED*. Different letters indicate statistically significant differences (Tukey test P value < 0.05).

1.2 Supplementary Tables

Supplemental Table 1: PCA Correlation Values

Gene	PC1	PC2
AHA1	**0,86**	-0,13
AHA2	**0,89**	-0,26
BES1	-0,64	-0,47
CESA1	**0,71**	-0,47
CESA3	**0,88**	0,14
CESA6	**0,71**	-0,38
CSLA9	0,18	**-0,81**
COBRA	0,05	**-0,9**
CPD	-0,53	**-0,76**
CYCD3;1	**0,84**	0,04
DWF4	-0,42	**-0,81**
EXPA1	0,27	0,1
PLL12	**0,8**	-0,09
TTL3	**0,9**	-0,03

Supplemental Table 2. Two-way ANOVA analysis followed by a mean comparison test was used to identify significant differences (P value < 0.05) between root growth rates of Col-0 and *ttl1* in osmotic shock and osmotic gradient using R Software. A. Two-way ANOVA. B. Mean comparison test in osmotic gradient. C. Mean comparison test in osmotic shock.

```
###  Osmotic Gradient #################

mod.1_gr1 <- lm ( b1 ~ genotype + media + genotype * media, data = df.gradient )

Analysis of Variance Table

Response: b1
               Df  Sum Sq  Mean Sq F value    Pr(>F)    
genotype        1 0.03426 0.034257  3.9045   0.05055 .  
media           3 0.74667 0.248890 28.3678 8.363e-14 ***
genotype:media  3 0.02037 0.006789  0.7738   0.51095    
Residuals     115 1.00897 0.008774                      
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

```
###  Osmotic Shock #################
anova (mod.1_shock)
Analysis of Variance Table

Response: b1
              Df Sum Sq Mean Sq  F value  Pr(>F)
genotype        1 0.0252 0.02518   4.1689 0.04276 *
media           2 3.3973 1.69866 281.2338 < 2e-16 ***
genotype:media   2 0.0086 0.00429   0.7109 0.49269
Residuals      165 0.9966 0.00604
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```

B. Mean comparison test in osmotic gradient.

contrast	**estimate**	**SE**	**df**	**t.ratio**	**p.value**
(Col-0 0_50mM) - ttl1 0_50mM	0.0714	0.0342	115	2.0878	0.4289
(Col-0 0_50mM) - (Col-0 200_300mM)	0.0307	0.0354	115	0.8661	0.9884
(Col-0 0_50mM) - ttl1 200_300mM	0.0780	0.0362	115	2.1526	0.3882
(Col-0 0_50mM) - (Col-0 300_400mM)	0.0664	0.0382	115	1.7384	0.6622
(Col-0 0_50mM) - ttl1 300_400mM	0.1431	0.0429	115	3.3383	0.0243
(Col-0 0_50mM) - (Col-0 Control)	-0.1024	0.0308	115	-3.3243	0.0254
(Col-0 0_50mM) - ttl1 Control	-0.0869	0.0302	115	-2.8816	0.0859
ttl1 0_50mM - (Col-0 200_300mM)	-0.0406	0.0355	115	-1.1457	0.9450
ttl1 0_50mM - ttl1 200_300mM	0.0067	0.0363	115	0.1842	0.9999
ttl1 0_50mM - (Col-0 300_400mM)	-0.0049	0.0382	115	-0.1289	0.9999
ttl1 0_50mM - ttl1 300_400mM	0.0717	0.0429	115	1.6728	0.7045
ttl1 0_50mM - (Col-0 Control)	-0.1739	0.0308	115	-5.6406	3.3817 e-6
ttl1 0_50mM - ttl1 Control	-0.1583	0.0302	115	-5.2490	1.9192 e-5
(Col-0 200_300mM) - ttl1 200_300mM	0.0474	0.0375	115	1.2628	0.9104
(Col-0 200_300mM) - (Col-0 300_400mM)	0.0357	0.0394	115	0.9070	0.9849
(Col-0 200_300mM) - ttl1 300_400mM	0.1123	0.0439	115	2.5594	0.1819
(Col-0 200_300mM) - (Col-0 Control)	-0.1332	0.0323	115	-4.1304	0.0017
(Col-0 200_300mM) - ttl1 Control	-0.1176	0.0316	115	-3.7212	0.0072
ttl1 200_300mM - (Col-0 300_400mM)	-0.0116	0.0401	115	-0.2896	0.9999
ttl1 200_300mM - ttl1 300_400mM	0.0650	0.0445	115	1.4599	0.8267
ttl1 200_300mM - (Col-0 Control)	-0.1805	0.0331	115	-5.4529	7.8417 e-6
ttl1 200_300mM - ttl1 Control	-0.1650	0.0325	115	-5.0778	4.0054 e-5

(Col-0 300_400mM) - ttl1 300_400mM	0.0766	0.0462	115	1.66059	0.7122
(Col-0 300_400mM) - (Col-0 Control)	-0.1689	0.0353	115	-4.7927	1.3163 e-4
(Col-0 300_400mM) - ttl1 Control	-0.1534	0.0347	115	-4.4240	5.7103 e-4
ttl1 300_400mM - (Col-0 Control)	-0.2456	0.0402	115	-6.1045	3.9644 e-7
ttl1 300_400mM - ttl1 Control	-0.2300	0.0397	115	-5.7907	1.7065 e-6
(Col-0 Control) - ttl1 Control	0.0155	0.0263	115	0.5924	0.9989

C. Mean comparison test in osmotic shock.

contrast	estimate	SE	df	t.ratio	p.value
(Col-0 0.3M) - ttl1 0.3M	0.0497	0.0196	165	2.5371	0.1195
(Col-0 0.3M) - (Col-0 0.4M)	0.1457	0.0202	165	7.1980	3.0669 e-10
(Col-0 0.3M) - ttl1 0.4M	0.1738	0.0204	165	8.5099	1.7131 e-13
(Col-0 0.3M) - (Col-0 Control)	-0.2007	0.0213	165	-9.4322	1.6542 e-14
(Col-0 0.3M) - ttl1 Control	-0.1852	0.0206	165	-8.9825	2.5091 e-14
ttl1 0.3M - (Col-0 0.4M)	0.0959	0.0198	165	4.8499	4.1408 e-5
ttl1 0.3M - ttl1 0.4M	0.1240	0.0199	165	6.2121	6.1276 e-8
ttl1 0.3M - (Col-0 Control)	-0.2505	0.0208	165	-12.0145	0
ttl1 0.3M - ttl1 Control	-0.2349	0.0202	165	-11.6487	0
(Col-0 0.4M) - ttl1 0.4M	0.0281	0.0206	165	1.3651	0.7477
(Col-0 0.4M) - (Col-0 Control)	-0.3464	0.0214	165	-16.1535	0
(Col-0 0.4M) - ttl1 Control	-0.3309	0.0208	165	-15.9192	0
ttl1 0.4M - (Col-0 Control)	-0.3745	0.0216	165	-17.3247	0
ttl1 0.4M - ttl1 Control	-0.3589	0.0209	165	-17.1248	0
(Col-0 Control) - ttl1 Control	0.0157	0.0218	165	0.7139	0.9800

Supplemental Table 3. Primer’s sequences used in RT-qPCR analysis in this study.

Gene to amplify	**Primer sequence**
Actin 2 (AT3G18780)	Fw: 5’ - CGT ACA ACC GGT ATT GTG CTG GAT -3’
	Rv: 5’ – GCT TGG TGC AAG TGC TGT GAT TTC- 3’
Cytochrome C oxidase related (AT4G37830)	Fw: 5’- GCG ATT GTA CGT TCA GCT CTT TC-3'
	Rv: 5’- GTG CTC TTT GTT GTG CTT CAC C-3’
CESA1 (AT4G32410)	Fw: 5’- TCA TCA TAC CCG AGA TAA GCA AC-3’

	Rv: 5’- ACG ACT GGT AGC CAA CTG TTT AC-3’
CESA3 (AT5G05170)	Fw: 5’- CGT GCT GAC AGG ACC AGT ATT-3’
	Rv: 5’- CTT ACT CGT GGG AAG GGA GAG G-3’
CESA6 (AT5G64740)	Fw: 5’- ACA GCA CAG AAA GTG CCT GAG-3’
	Rv: 5’- GGA GCA TTT GAT AGA ACC CCA-3'
TTL1 (AT1G53300)	Fw: 5'- GCT AGC CAA ATC GAT CCA AG-3’
	Rv: 5’-AGC TCC CCA TCT TTC CAT CT-3’
TTL3 (AT2G42580)	Fw:5’- ATG GTG GAT GTG GAG GAG AG-3’
	Rv: 5’- AGC AGA GCC AAA CTC CAA AA-3’
PECTATE LYASE12 (AT5G04310)	Fw: 5'-CGG AAG GTG ACG TTA TGG TT-3'
	Rv: 5’-TCA ATG TGA AAA GCC CAT CA-3'
CSLA9 (AT5G03760)	Fw: 5'-TCG GTT TAC TCG AAG GAG GA-3
	Rv: 5’-GAT TGC TTG TGC GAA AAG GT-3'
EXPANSIN A1 (AT1G69530)	Fw: 5'-AAG GCT ATG GAA CCA ACA CG-3
	Rv: 5’-ATT TTC GCC ACT GGA ATT G-3’
AHA1 (AT2G18960)	Fw: 5'-AAT TTT CGC CAC TGG AAT TG-3'
	Rv: 5’-ACC AAC TCC TTG ACC TGG TG-3'
AHA2 (AT4G30190)	Fw: 5'-TGC TCA AAG GAC ACT TCA CG-3'
	Rv: 5’GCC CTT TAG CTT CAC GAC TG-3'
CYCD3:1 (AT4G34160)	Fw: 5'-CCT CTC TGT AAT CTC CGA TTC AA-3'
	Rv: 5’- AAA GGG TTT GCA TCA ATC ACG-3'
BES1 (AT1G19350)	Fw: 5'- CGA GTT GGT GAT CCA CAC AAT A-3'
	Rv: 5'-GGA GGA AGC GAT GAA GGA ATA C -3'
DWF4 (AT3G50660)	Fw: 5'- GTG GGT GGA AAG TGT TAC CG-3
	Rv: 5 -CTG TTG CCA TCT CCA AGG AT -3 '
CPD (AT5G05690)	Fw: 5'-AGC AAC TCG GTA ACG ACA GG-3'
	Rv: 5'- CAG AGA GTG CAA CCC TAG CC-3

Supplemental Table 4. One-way ANOVA Analysis of RT-qPCR data utilizing Excell for RT-qPCR expression data in Control Conditions P value threshold set at 0.05.

AHA1

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	3	3,08793661	1,0293122	0,08158929
ttl1	3	1,21384146	0,40461382	0,01006205

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,58537211	1	0,58537211	12,7738904	0,02329105	7,70864742
Within Groups	0,18330269	4	0,04582567			
Total	0,76867479	5				

AHA2

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	3	3,106764	1,035588	0,12241669
ttl1	3	0,75143775	0,25047925	0,00311039

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,92459362	1	0,92459362	14,7313811	0,01848878	7,70864742
Within Groups	0,25105416	4	0,06276354			

Total	1,17564778	5

BES1

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	2	1,6890286	0,8445143	0,00042008
ttl1	2	1,62164906	0,81082453	0,00067814

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,001135	1	0,001135	2,06698125	0,28709414	18,5128205
Within Groups	0,00109822	2	0,00054911			
Total	0,00223322	3				

CESA1

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	*3*	*3,02021514*	*1,00673838*	*0,0193292*
ttl1	*3*	*1,55438591*	*0,51812864*	*0,01400333*

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,35810922	1	0,35810922	21,4870704	0,00976749	7,70864742
Within Groups	0,06666506	4	0,01666627			
Total	0,42477428	5				

CESA3

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*

Col-0	3	3,04324076	1,01441359	0,04341288
ttl1	3	2,54317742	0,84772581	0,08493571

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,04167722	1	0,04167722	0,64943795	0,46549338	7,70864742
Within Groups	0,25669719	4	0,0641743			
Total	0,29837442	5				

CESA6

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	3	3,02844704	1,00948235	0,02862059
ttl1	3	1,3998204	0,4666068	0,00939779

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,44207079	1	0,44207079	23,2556326	0,0085081	7,70864742
Within Groups	0,07603677	4	0,01900919			
Total	0,51810756	5				

CSLA9

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	3	3,0595446	1,0198482	0,06582644
ttl1	3	1,91480552	0,63826851	0,01706182

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,21840459	1	0,21840459	5,26985584	0,08334005	7,70864742

Within Groups	0,16577652	4	0,04144413
Total	0,38418112	5	

COBRA

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	2	1,99051563	0,99525782	0,00033018
ttl1	2	0,9528354	0,4764177	0,00560215

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,26919506	1	0,26919506	90,7552401	0,01083981	18,5128205
Within Groups	0,00593233	2	0,00296617			
Total	0,27512739	3				

CPD

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	3	3,00316012	1,00105337	0,00318405
ttl1	3	2,06363494	0,68787831	0,00656861

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,14711793	1	0,14711793	30,1698142	0,0053537	7,70864742
Within Groups	0,01950531	4	0,00487633			
Total	0,16662324	5				

CYCD3;1

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	3	3,01472769	1,00490923	0,0153924
ttl1	3	1,77698094	0,59232698	0,00626806

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,25533617	1	0,25533617	23,5762504	0,00830606	7,70864742
Within Groups	0,04332091	4	0,01083023			
Total	0,29865708	5				

DWF4

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	3	3,06292863	1,02097621	0,06990463
ttl1	3	1,18859848	0,39619949	0,00515324

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,58551892	1	0,58551892	15,6017998	0,01681926	7,70864742
Within Groups	0,15011574	4	0,03752893			
Total	0,73563466	5				

EXPA1

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	3	3,04672516	1,01557505	0,04849267
ttl1	3	3,24890585	1,08296862	0,07491119

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,00681284	1	0,00681284	0,11041533	0,75635536	7,70864742
Within Groups	0,24680771	4	0,06170193			
Total	0,25362055	5				

TTL3

Anova: Single Factor

SUMMARY

Groups	*Count*	*Sum*	*Average*	*Variance*
Col-0	2	1,99429909	0,99714954	0,01045787
ttl1	2	1,81119124	0,90559562	0,07766462

ANOVA

Source of Variation	*SS*	*df*	*MS*	*F*	*P-value*	*F crit*
Between Groups	0,00838212	1	0,00838212	0,19023795	0,70528454	18,5128205
Within Groups	0,08812249	2	0,04406125			
Total	0,09650461	3				

Supplemental Table 5. ANOVA Analysis of RT-qPCR data utilizing INFOSTAT with a multiple testing corrected P value threshold set at 0.05.

```
New table : 2/5/2024 - 4:56:51 PM - [Version : 4/30/2020]

Gen  Variable N   R²  Adj R²  CV
AHA1 lfc      18 0.91   0.87 13.42

Analysis of variance table (Partial SS)
      S.V.          SS  df  MS    F    p-value
Model              3.13  5 0.63 24.08 <0.0001
Condicion          2.38  2 1.19 45.83 <0.0001
Genotipo           0.01  1 0.01  0.51  0.4902
Condicion*Genotipo 0.73  2 0.37 14.11  0.0007
Error              0.31 12 0.03
Total              3.44 17

Test:Tukey Alpha:=0.05 LSD:=0.24826
Error: 0.0260 df: 12
Condicion Means n  S.E.
```

```
Control     0.72  6 0.07 A
shock       1.29  6 0.07    B
gradiente   1.59  6 0.07       C
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.16554
Error: 0.0260 df: 12
Genotipo Means n  S.E.
ttl1      1.17  9 0.05 A
Col-0     1.23  9 0.05 A
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.44203
Error: 0.0260 df: 12
Condicion Genotipo Means n  S.E.
Control   ttl1      0.40  3 0.09 A
Control   Col-0     1.03  3 0.09    B
shock     Col-0     1.18  3 0.09    B  C
shock     ttl1      1.40  3 0.09    B  C  D
gradiente Col-0     1.47  3 0.09       C  D
gradiente ttl1      1.72  3 0.09          D
Means with a common letter are not significantly different (p > 0.05)



Gen  Variable N   R²  Adj R²  CV
AHA2 lfc      18 0.93   0.91 17.65

Analysis of variance table (Partial SS)
      S.V.            SS  df  MS   F    p-value
Model                4.80  5 0.96 33.57 <0.0001
Condicion            3.72  2 1.86 65.08 <0.0001
Genotipo             0.11  1 0.11  3.73  0.0773
Condicion*Genotipo 0.97  2 0.49 16.98  0.0003
Error                0.34 12 0.03
Total                5.14 17

Test:Tukey Alpha:=0.05 LSD:=0.26035
Error: 0.0286 df: 12
Condicion Means n  S.E.
shock       0.63  6 0.07 A
Control     0.64  6 0.07 A
gradiente   1.60  6 0.07    B
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.17361
Error: 0.0286 df: 12
Genotipo Means n  S.E.
ttl1      0.88  9 0.06 A
Col-0     1.03  9 0.06 A
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.46357
Error: 0.0286 df: 12
```

```
Condicion Genotipo Means n  S.E.
Control   ttl1      0.25  3 0.10 A
shock     Col-0     0.47  3 0.10 A  B
shock     ttl1      0.79  3 0.10    B  C
Control   Col-0     1.04  3 0.10       C
gradiente Col-0     1.60  3 0.10          D
gradiente ttl1      1.60  3 0.10          D
Means with a common letter are not significantly different (p > 0.05)
```

```
Gen  Variable N   R²  Adj R²  CV
BES1 lfc      18 0.67    0.53 21.85
```

Analysis of variance table (Partial SS)

```
      S.V.           SS   df  MS    F    p-value
Model              0.73  5 0.15  4.90  0.0113
Condicion          0.67  2 0.34 11.27  0.0018
Genotipo           0.02  1 0.02  0.60  0.4539
Condicion*Genotipo 0.04  2 0.02  0.67  0.5297
Error              0.36 12 0.03
Total              1.09 17
```

Test:Tukey Alpha:=0.05 LSD:=0.26651

```
Error: 0.0299 df: 12
Condicion Means n  S.E.
gradiente  0.52  6 0.07 A
shock      0.91  6 0.07    B
control    0.94  6 0.07    B
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.17772

```
Error: 0.0299 df: 12
Genotipo Means n  S.E.
ttl1      0.76  9 0.06 A
Col-0     0.82  9 0.06 A
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.47454

```
Error: 0.0299 df: 12
Condicion Genotipo Means n  S.E.
gradiente ttl1      0.48  3 0.10 A
gradiente Col-0     0.55  3 0.10 A
control   ttl1      0.85  3 0.10 A  B
shock     Col-0     0.89  3 0.10 A  B
shock     ttl1      0.94  3 0.10 A  B
control   Col-0     1.03  3 0.10    B
Means with a common letter are not significantly different (p > 0.05)
```

```
 Gen  Variable N   R²  Adj R²  CV
CESA1 lfc      18 0.63    0.48 21.67
```

Analysis of variance table (Partial SS)

```
      S.V.           SS   df  MS    F   p-value
```

```
Model                0.82  5 0.16 4.14  0.0203
Condicion            0.34  2 0.17 4.26  0.0400
Genotipo             0.03  1 0.03 0.83  0.3794
Condicion*Genotipo 0.45  2 0.22 5.68  0.0184
Error                0.47 12 0.04
Total                1.29 17
```

Test:Tukey Alpha:=0.05 LSD:=0.30605

```
Error: 0.0395 df: 12
Condicion Means n  S.E.
Control     0.76  6 0.08 A
shock       0.89  6 0.08 A  B
gradiente  1.09  6 0.08     B
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.20408

```
Error: 0.0395 df: 12
Genotipo Means n  S.E.
ttl1       0.87  9 0.07 A
Col-0      0.96  9 0.07 A
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.54493

```
Error: 0.0395 df: 12
Condicion Genotipo Means n  S.E.
Control   ttl1       0.52  3 0.11 A
shock     Col-0      0.75  3 0.11 A  B
Control   Col-0      1.01  3 0.11 A  B
shock     ttl1       1.03  3 0.11 A  B
gradiente ttl1       1.07  3 0.11     B
gradiente Col-0      1.12  3 0.11     B
Means with a common letter are not significantly different (p > 0.05)
```

```
 Gen  Variable N   R²  Adj R²  CV
CESA3 lfc      18 0.66   0.52 32.92
```

Analysis of variance table (Partial SS)

```
      S.V.             SS  df  MS   F   p-value
Model                4.26  5 0.85 4.63  0.0138
Condicion            1.71  2 0.85 4.64  0.0321
Genotipo             1.24  1 1.24 6.74  0.0234
Condicion*Genotipo 1.31  2 0.65 3.56  0.0610
Error                2.21 12 0.18
Total                6.46 17
```

Test:Tukey Alpha:=0.05 LSD:=0.66028

```
Error: 0.1838 df: 12
Condicion Means n  S.E.
Control     0.93  6 0.18 A
shock       1.29  6 0.18 A  B
gradiente  1.69  6 0.18     B
Means with a common letter are not significantly different (p > 0.05)
```

```
Test:Tukey Alpha:=0.05 LSD:=0.44029
Error: 0.1838 df: 12
Genotipo Means n  S.E.
Col-0     1.04  9 0.14 A
ttl1      1.56  9 0.14    B
Means with a common letter are not significantly different (p > 0.05)
```

```
Test:Tukey Alpha:=0.05 LSD:=1.17566
Error: 0.1838 df: 12
Condicion Genotipo Means n  S.E.
Control   ttl1      0.85  3 0.25 A
shock     Col-0     0.99  3 0.25 A
Control   Col-0     1.01  3 0.25 A
gradiente Col-0     1.11  3 0.25 A  B
shock     ttl1      1.59  3 0.25 A  B
gradiente ttl1      2.26  3 0.25    B
Means with a common letter are not significantly different (p > 0.05)
```

```
 Gen  Variable N   R²  Adj R²  CV
CESA6 lfc      18 0.77   0.67 25.59
```

```
Analysis of variance table (Partial SS)
      S.V.               SS    df   MS      F    p-value
Model                    1.68  5     0.34  7.89  0.0017
Condicion                0.98  2     0.49 11.46  0.0016
Genotipo              1.2E-03  1 1.2E-03  0.03  0.8705
Condicion*Genotipo       0.70  2     0.35  8.24  0.0056
Error                    0.51 12     0.04
Total                    2.20 17
```

```
Test:Tukey Alpha:=0.05 LSD:=0.31824
Error: 0.0427 df: 12
Condicion Means n  S.E.
shock      0.56  6 0.08 A
Control    0.74  6 0.08 A
gradiente  1.12  6 0.08    B
Means with a common letter are not significantly different (p > 0.05)
```

```
Test:Tukey Alpha:=0.05 LSD:=0.21221
Error: 0.0427 df: 12
Genotipo Means n  S.E.
Col-0     0.80  9 0.07 A
ttl1      0.82  9 0.07 A
Means with a common letter are not significantly different (p > 0.05)
```

```
Test:Tukey Alpha:=0.05 LSD:=0.56663
Error: 0.0427 df: 12
Condicion Genotipo Means n  S.E.
shock     Col-0     0.41  3 0.12 A
Control   ttl1      0.47  3 0.12 A  B
shock     ttl1      0.71  3 0.12 A  B  C
gradiente Col-0     0.97  3 0.12 A  B  C
Control   Col-0     1.01  3 0.12    B  C
```

```
gradiente ttl1       1.27  3 0.12        C
Means with a common letter are not significantly different (p > 0.05)


 Gen  Variable N   R²  Adj R²  CV
CESA9 lfc      18 0.57   0.39 24.85

Analysis of variance table (Partial SS)
      S.V.             SS  df  MS   F    p-value
Model                 0.54  5 0.11 3.15  0.0480
Condicion             0.10  2 0.05 1.46  0.2714
Genotipo              0.03  1 0.03 0.75  0.4040
Condicion*Genotipo 0.41  2 0.21 6.04  0.0153
Error                 0.41 12 0.03
Total                 0.94 17

Test:Tukey Alpha:=0.05 LSD:=0.28393
Error: 0.0340 df: 12
Condicion Means n  S.E.
shock       0.65  6 0.08 A
gradiente   0.75  6 0.08 A
Control     0.83  6 0.08 A
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.18933
Error: 0.0340 df: 12
Genotipo Means n  S.E.
ttl1       0.70  9 0.06 A
Col-0      0.78  9 0.06 A
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.50554
Error: 0.0340 df: 12
Condicion Genotipo Means n  S.E.
shock     Col-0      0.48  3 0.11 A
Control   ttl1       0.64  3 0.11 A  B
gradiente ttl1       0.66  3 0.11 A  B
shock     ttl1       0.82  3 0.11 A  B
gradiente Col-0      0.84  3 0.11 A  B
Control   Col-0      1.02  3 0.11    B
Means with a common letter are not significantly different (p > 0.05)


 Gen  Variable N   R²  Adj R²  CV
COBRA lfc      18 0.79   0.70 15.42

Analysis of variance table (Partial SS)
      S.V.             SS  df  MS    F     p-value
Model                 0.56  5 0.11  8.89  0.0010
Condicion             0.04  2 0.02  1.56  0.2493
Genotipo              0.06  1 0.06  4.84  0.0482
Condicion*Genotipo 0.46  2 0.23 18.23  0.0002
Error                 0.15 12 0.01
Total                 0.71 17
```

```
Test:Tukey Alpha:=0.05 LSD:=0.17269
Error: 0.0126 df: 12
Condicion Means n  S.E.
gradiente  0.66  6 0.05 A
control    0.76  6 0.05 A
shock      0.76  6 0.05 A
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.11515
Error: 0.0126 df: 12
Genotipo Means n  S.E.
ttl1      0.67  9 0.04 A
Col-0     0.79  9 0.04    B
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.30748
Error: 0.0126 df: 12
Condicion Genotipo Means n  S.E.
control   ttl1      0.52  3 0.06 A
gradiente ttl1      0.58  3 0.06 A
shock     Col-0     0.61  3 0.06 A  B
gradiente Col-0     0.74  3 0.06 A  B  C
shock     ttl1      0.91  3 0.06    B  C
control   Col-0     1.00  3 0.06       C
Means with a common letter are not significantly different (p > 0.05)



Gen Variable N   R²  Adj R²  CV
CPD lfc      18 0.84   0.78 11.50

Analysis of variance table (Partial SS)
      S.V.           SS  df  MS   F    p-value
Model               0.41  5 0.08 12.85  0.0002
Condicion           0.22  2 0.11 17.44  0.0003
Genotipo            0.13  1 0.13 20.61  0.0007
Condicion*Genotipo  0.06  2 0.03  4.38  0.0373
Error               0.08 12 0.01
Total               0.49 17

Test:Tukey Alpha:=0.05 LSD:=0.12308
Error: 0.0064 df: 12
Condicion Means n  S.E.
gradiente  0.58  6 0.03 A
shock      0.66  6 0.03 A
Control    0.84  6 0.03    B
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.08207
Error: 0.0064 df: 12
Genotipo Means n  S.E.
ttl1      0.61  9 0.03 A
Col-0     0.78  9 0.03    B
Means with a common letter are not significantly different (p > 0.05)
```

```
Test:Tukey Alpha:=0.05 LSD:=0.21915
Error: 0.0064 df: 12
Condicion Genotipo Means n  S.E.
gradiente ttl1      0.50  3 0.05 A
shock     ttl1      0.64  3 0.05 A
gradiente Col-0     0.66  3 0.05 A
shock     Col-0     0.68  3 0.05 A
Control   ttl1      0.69  3 0.05 A
Control   Col-0     1.00  3 0.05    B
Means with a common letter are not significantly different (p > 0.05)
```

```
  Gen    Variable N   R²  Adj R²  CV
CYCD3;1 lfc      18 0.83    0.75 30.31
```

```
Analysis of variance table (Partial SS)
      S.V.          SS   df  MS    F    p-value
Model              20.77  5 4.15 11.37  0.0003
Condicion          18.56  2 9.28 25.40 <0.0001
Genotipo            1.47  1 1.47  4.04  0.0676
Condicion*Genotipo  0.73  2 0.37  1.00  0.3951
Error               4.39 12 0.37
Total              25.16 17
```

```
Test:Tukey Alpha:=0.05 LSD:=0.93120
Error: 0.3655 df: 12
Condicion Means n  S.E.
Control    0.80  6 0.25 A
shock      1.90  6 0.25    B
gradiente  3.28  6 0.25       C
Means with a common letter are not significantly different (p > 0.05)
```

```
Test:Tukey Alpha:=0.05 LSD:=0.62095
Error: 0.3655 df: 12
Genotipo Means n  S.E.
ttl1      1.71  9 0.20 A
Col-0     2.28  9 0.20 A
Means with a common letter are not significantly different (p > 0.05)
```

```
Test:Tukey Alpha:=0.05 LSD:=1.65804
Error: 0.3655 df: 12
Condicion Genotipo Means n  S.E.
Control   ttl1      0.59  3 0.35 A
Control   Col-0     1.00  3 0.35 A
shock     ttl1      1.81  3 0.35 A  B
shock     Col-0     1.99  3 0.35 A  B
gradiente ttl1      2.72  3 0.35    B  C
gradiente Col-0     3.84  3 0.35       C
Means with a common letter are not significantly different (p > 0.05)
```

```
Gen  Variable N   R²  Adj R²  CV
```

```
DWF4 lfc       18 0.86    0.80 28.67
```

Analysis of variance table (Partial SS)

```
      S.V.            SS  df  MS   F     p-value
Model                1.21  5 0.24 14.31  0.0001
Condicion            0.61  2 0.31 18.07  0.0002
Genotipo             0.22  1 0.22 12.71  0.0039
Condicion*Genotipo 0.38  2 0.19 11.34  0.0017
Error                0.20 12 0.02
Total                1.41 17
```

Test:Tukey Alpha:=0.05 LSD:=0.20047

Error: 0.0169 df: 12

```
Condicion Means n  S.E.
gradiente  0.28  6 0.05 A
shock      0.38  6 0.05 A
Control    0.71  6 0.05    B
```

Means with a common letter are not significantly different (p > 0.05)

Test:Tukey Alpha:=0.05 LSD:=0.13368

Error: 0.0169 df: 12

```
Genotipo Means n  S.E.
ttl1      0.34  9 0.04 A
Col-0     0.56  9 0.04    B
```

Means with a common letter are not significantly different (p > 0.05)

Test:Tukey Alpha:=0.05 LSD:=0.35694

Error: 0.0169 df: 12

```
Condicion Genotipo Means n  S.E.
gradiente ttl1      0.24  3 0.08 A
gradiente Col-0     0.32  3 0.08 A
shock     Col-0     0.35  3 0.08 A
Control   ttl1      0.40  3 0.08 A
shock     ttl1      0.40  3 0.08 A
Control   Col-0     1.02  3 0.08    B
```

Means with a common letter are not significantly different (p > 0.05)

```
 Gen  Variable N   R²  Adj R²  CV
EXPA1 lfc       18 0.84    0.77 15.81
```

Analysis of variance table (Partial SS)

```
      S.V.            SS  df  MS   F     p-value
Model                2.80  5 0.56 12.26  0.0002
Condicion            1.39  2 0.69 15.15  0.0005
Genotipo             0.81  1 0.81 17.81  0.0012
Condicion*Genotipo 0.60  2 0.30   6.58  0.0118
Error                0.55 12 0.05
Total                3.35 17
```

Test:Tukey Alpha:=0.05 LSD:=0.32927

Error: 0.0457 df: 12

```
Condicion Means n  S.E.
Control    1.05  6 0.09 A
```

```
gradiente  1.29  6 0.09 A
shock      1.72  6 0.09    B
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.21957

```
Error: 0.0457 df: 12
Genotipo Means n  S.E.
Col-0     1.14  9 0.07 A
ttl1      1.57  9 0.07    B
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.58629

```
Error: 0.0457 df: 12
Condicion Genotipo Means n  S.E.
Control   Col-0     1.02  3 0.12 A
Control   ttl1      1.08  3 0.12 A
gradiente Col-0     1.15  3 0.12 A
shock     Col-0     1.26  3 0.12 A
gradiente ttl1      1.43  3 0.12 A
shock     ttl1      2.18  3 0.12    B
Means with a common letter are not significantly different (p > 0.05)
```

```
     Gen       Variable N   R²  Adj R²  CV
Pectato liasa lfc      18 0.81   0.72 19.21
```

Analysis of variance table (Partial SS)

```
      S.V.              SS     df    MS      F    p-value
Model                    1.95  5     0.39  9.94  0.0006
Condicion                1.70  2     0.85 21.54  0.0001
Genotipo              4.3E-03  1 4.3E-03  0.11  0.7457
Condicion*Genotipo       0.26  2     0.13  3.24  0.0749
Error                    0.47 12     0.04
Total                    2.43 17
```

Test:Tukey Alpha:=0.05 LSD:=0.30554

```
Error: 0.0393 df: 12
Condicion Means n  S.E.
shock      0.77  6 0.08 A
control    0.86  6 0.08 A
gradiente  1.46  6 0.08    B
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.20374

```
Error: 0.0393 df: 12
Genotipo Means n  S.E.
Col-0     1.02  9 0.07 A
ttl1      1.05  9 0.07 A
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.54403

```
Error: 0.0393 df: 12
Condicion Genotipo Means n  S.E.
```

```
shock     Col-0     0.70  3 0.11 A
control   ttl1      0.71  3 0.11 A
shock     ttl1      0.85  3 0.11 A  B
control   Col-0     1.01  3 0.11 A  B
gradiente Col-0     1.34  3 0.11    B  C
gradiente ttl1      1.59  3 0.11       C
Means with a common letter are not significantly different (p > 0.05)


Gen  Variable N  R² Adj R²  CV
TTL1 lfc       9 nd   0.42 20.44

Analysis of variance table (Partial SS)
      S.V.          SS  df  MS   F    p-value
Model              0.22  2 0.11 3.90  0.0822
Condicion          0.22  2 0.11 3.90  0.0822
Genotipo           0.00  0 0.00   nd      nd
Condicion*Genotipo 0.00  0 0.00   nd      nd
Error              0.17  6 0.03
Total              0.39  8

Test:Tukey Alpha:=0.05 LSD:=0.41962
Error: 0.0281 df: 6
Condicion Means n         S.E.
shock      0.63  3  1.7480142918471E45 A
gradiente  0.82  3 1.71640702665233E30 A
control    1.01  3  1.7480142918471E45 A
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.41962
Error: 0.0281 df: 6
Genotipo Means n         S.E.
Col-0     0.82  9 5.17516190448665E29 A
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=0.41962
Error: 0.0281 df: 6
Condicion Genotipo Means n         S.E.
shock     Col-0     0.63  3  1.7480142918471E45 A
gradiente Col-0     0.82  3 1.71640702665233E30 A
control   Col-0     1.01  3  1.7480142918471E45 A
Means with a common letter are not significantly different (p > 0.05)


Gen  Variable N   R²  Adj R²  CV
TTL3 lfc      18 0.85   0.78 15.63

Analysis of variance table (Partial SS)
      S.V.            SS    df    MS      F     p-value
Model                 2.93  5     0.59 13.20  0.0002
Condicion             2.36  2     1.18 26.62 <0.0001
Genotipo           1.4E-03  1 1.4E-03  0.03  0.8613
Condicion*Genotipo    0.57  2     0.28  6.37  0.0130
Error                 0.53 12     0.04
```

```
Total                 3.46 17
```

Test:Tukey Alpha:=0.05 LSD:=0.32453

```
Error: 0.0444 df: 12
Condicion Means n  S.E.
Control     0.93  6 0.09 A
shock       1.31  6 0.09    B
gradiente   1.81  6 0.09       C
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.21640

```
Error: 0.0444 df: 12
Genotipo Means n  S.E.
Col-0      1.34  9 0.07 A
ttl1       1.36  9 0.07 A
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=0.57784

```
Error: 0.0444 df: 12
Condicion Genotipo Means n  S.E.
Control   ttl1      0.85  3 0.12 A
Control   Col-0     1.00  3 0.12 A  B
shock     Col-0     1.05  3 0.12 A  B
shock     ttl1      1.57  3 0.12    B  C
gradiente ttl1      1.66  3 0.12       C
gradiente Col-0     1.96  3 0.12       C
Means with a common letter are not significantly different (p > 0.05)
```

```
Gen  Variable N   R²  Adj R²  CV
TTL4 lfc      18 0.55   0.36 38.01
```

Analysis of variance table (Partial SS)

```
      S.V.          SS   df  MS    F   p-value
Model              28.88  5  5.78 2.95  0.0577
Condicion          21.24  2 10.62 5.43  0.0209
Genotipo            6.43  1  6.43 3.29  0.0949
Condicion*Genotipo  1.22  2  0.61 0.31  0.7385
Error              23.47 12  1.96
Total              52.35 17
```

Test:Tukey Alpha:=0.05 LSD:=2.15402

```
Error: 1.9557 df: 12
Condicion Means n  S.E.
control     2.67  6 0.57 A
gradiente   3.19  6 0.57 A  B
shock       5.19  6 0.57    B
Means with a common letter are not significantly different (p > 0.05)
```

Test:Tukey Alpha:=0.05 LSD:=1.43635

```
Error: 1.9557 df: 12
Genotipo Means n  S.E.
Col-0      3.08  9 0.47 A
ttl1       4.28  9 0.47 A
```

```
Means with a common letter are not significantly different (p > 0.05)


Test:Tukey Alpha:=0.05 LSD:=3.83531
Error: 1.9557 df: 12
Condicion Genotipo Means n  S.E.
control   Col-0     2.11  3 0.81 A
gradiente Col-0     2.89  3 0.81 A  B
control   ttl1      3.23  3 0.81 A  B
gradiente ttl1      3.48  3 0.81 A  B
shock     Col-0     4.25  3 0.81 A  B
shock     ttl1      6.12  3 0.81    B
Means with a common letter are not significantly different (p > 0.05)
```